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Fig. 11-2

401 CTCTACTGGAACGCACTTCTGTGAGGTTGAACAGATAAGGAATGGACCT 450
401 CTCTACTGGAACGCACTTCTGTGAGGTTGAACAGATAAGGAATGGACCT 450
451 CCAGTCATTTCATTCTGGAATCAAAGACCTAAAAGTCTTGAAAACAACCCA 500
451 CCAGTCATTTCATTCTGGAATCAAAGACCTAAAAGTCTTGAAAACAACCCA 500
501 GTCTGGCTTTGAAGGATTCATCAAGGACCAGTTCACCACCCTCCCTGAGG 550
501 GTCTGGCTTTGAAGGATTCATCAAGGACCAGTTCACCACCCTCCCTGAGG 550
551 TGAAGGACCGGTGCTTTGCCACCCAAGTGTACTGCAAAATGGCGCTACCC 600
551 TGAAGGACCGGTGCTTTGCCACCCAAGTGTACTGCAAAATGGCGCTACCC 600
601 CAGGGCAGAGATGTGGACTTTGAGGCCACCTGGGACACTGTTAGGAGCAT 650
601 CAGGGCAGAGATGTGGACTTTGAGGCCACCTGGGACACTGTTAGGAGCAT 650
651 TGTCTGCAGAAAATTTGCTGGGCCCTATGACAAAGGCGAGTACTCGCCCT 700
651 TGTCTGCAGAAAATTTGCTGGGCCCTATGACAAAGGCGAGTACTCGCCCT 700
701 CTGTCCAGAAGACACTCTATGACATCCAGGTGCTCACCTGGGCCAGGTT 750
701 CTGTCCAGAAGACACTCTATGACATCCAGGTGCTCACCTGGGCCAGGTT 750
751 CCTGAGATAGAAGATATGAAAATCAGCCTGCCAAATATTTACTACTTAAA 800
751 CCTGAGATAGAAGATATGAAAATCAGCCTGCCAAATATTTACTACTTAAA 800
801 CATAGACATGTCCAAAATGGGACTGATCAACAAGGAAGAGGTTCTGCTAC 850
801 CATAGACATGTCCAAAATGGGACTGATCAACAAGGAAGAGGTTCTGCTAC 850
851 CTTTtagacaATCCATATGGAAAAATTACTGGTACAGTCAAGAGGAAGTTG 900
851 CTTTtagacaATCCATATGGCAGGATTACTGGTACAGTCAAGAGGAAGCTG 900
901 TCTTCAAGACTGTGA 915
901 ACTTCAAGGCTGTGA 915

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Fig. 12-1

Bestfit (GCG software) comparison of coding sequences of the cDNAs of Pig KS uricase ("PKS") vs. baboon uricase

"Pig KS" uricase:

Pig cDNA from 1 to 864 (NdeI site) and then Baboon 865 to 915 (end)

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	-9.000
Quality:	7573	Length:	915
Ratio:	8.277	Gaps:	0
Percent Similarity:	90.929	Percent Identity:	90.929

Match display thresholds for the alignment(s):

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| = IDENTITY
: = 5
. = 1

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pigKS.seq x baboon.seq July 25, 1998 10:21 ..

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PKS   1  ATGGGCTCATTACCGTAATGACTACAAAAAGAATGATGAGGTAGAGTTTGT  50
bab   1  ATGGCCGACTACCATACAACATAAAAAAGAATGATGAATTGGAGTTTGT  50

    51  CCGAACTGGCTATGGGAAGGATATGATAAAAGTTCTCCATATTCAGCGAG  100
    51  CCGAACTGGCTATGGGAAGGATATGGTAAAAAGTTCTCCATATTCAGCGAG  100

   101  ATGGAAATATCACAGCATTAAGAGGTGGCAACTTCAGTGCAACTGACT  150
   101  ATGGAAATATCACAGCATTAAGAGGTGGCAACTTCAGTGCAACTTACT  150

   151  TTGAGCTCCAAAAAGATTACCTGCATGGAGACAATTCAGATGTCATCCC  200
   151  CTGAGTTCCAAAAAGATTACCTGCATGGAGATAATTCAGATATCATCCC  200

   201  TACAGACACCATCAAGAACACAGTTAATGTCTTGGCGAAGTTCAAAGGCA  250
   201  TACAGACACCATCAAGAACACAGTTTCATGTCTTGGCAAAGTTTAAGGGAA  250

   251  TCAAAGCATAGAAACTTTTGCTGTGACTATCTGTGAGCATTTCCTTTCT  300
   251  TCAAAGCATAGAAGCCTTTGGTGTGAATATTTGTGAGTATTTTCTTTCT  300

   301  TCCTTCAAGCATGTTCATCAGAGCTCAAGTCTATGTGGAAGAAGTTCCCTTG  350
   301  TCTTTTAACCATGTAATCCGAGCTCAAGTCTACGTGGAAGAAATCCCTTG  350

   351  GAAGCGTTTGGAAAAGAATGGAGTTTAAGCATGTCCATGCATTATTATTATA  400
   351  GAAGCGCTTGAAAAGAATGGAGTTAAGCATGTCCATGCATTATTATCACA  400

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